

International Journal of Environment, Agriculture and Biotechnology

Vol-10, Issue-3; May-Jun, 2025

Peer-Reviewed International Journal

Journal Home Page Available: https://ijeab.com/

Journal DOI: 10.22161/ijeab



Genetic Variability of Quantitative Traits in Indian Mustard (*Brassica juncea* L.) Germplasm Lines

Himani Mehta, Neha and Ravindra Kumar

Mata Gujri College (Punjabi University, Patiala), Fatehgarh Sahib 140406, Punjab, India *Corresponding author

Received: 05 May 2025; Received in revised form: 03 Jun 2025; Accepted: 08 Jun 2025; Available online: 14 Jun 2025 ©2025 The Author(s). Published by Infogain Publication. This is an open-access article under the CC BY license (https://creativecommons.org/licenses/by/4.0/).

Abstract — The family Cruciferae (Brassicaceae) includes Indian mustard (Brassica juncea (L.) Czern & Coss), which is grown across India and the rest of the world under the genus Brassica. It contains 24% protein and 38–42% oil. Rai (B. juncea), a variety of mustard and rapeseed, is highly prized by farmers for its higher yield and stronger resistance to heat, relative diseases, lodging, shattering, drought circumstances, and saltwater sodic environments. In 50 genotypes of Indian mustard germplasm lines, an experiment was carried out to evaluate the genetic variability, correlation, and path analysis of twelve quantitative parameters. The experiment used a randomized block design with three replications. The analysis of variance ratios showed that the traits analyzed had highly significant differences among the genotypes. This indicates that there is considerable genetic variability among the Indian mustard germplasm lines for the quantitative traits under study. In conclusion, this study provides valuable insights into the genetic variability, heritability and genetic advance quantitative traits in Indian mustard germplasm lines.



Keywords— Heritability, genetic advance, Genetic Variability.

I. INTRODUCTION

Brassica juncea L., is a globally consumed vegetable, oilseed, and condiment (Saleem et al., 2017). It appears that mustard is a Brassicaceae family member. Two amphidiploid species (2n = 36) of Indian mustard are found in nature: B. nigra (2n = 16) and B. rapa (2n = 20). Mustard, the most common kind of Brassica, is cultivated in between 85 and 90 percent of all oilseed fields globally (Rao et al., 2017). Indian mustard, a significant oilseed crop, has been cultivated for thousands of years in China, India, and more recently, Australia. Its primary growth regions in India include Madhya Pradesh, Gujarat, Haryana, Uttar Pradesh, and Rajasthan (Sharma et al., 2020).

The majority of Indian mustard plants are self-pollinating, however between 5 and 30 percent of their growth depends on environmental factors and unintentional diversity pollinating insects. Amphidiploid Indian mustard is produced by normal chromosomal multiplication following an intraopen cross between Brassica compestris (2n=20) and Brassica nigra (2n=16) (Shrimali et al., 2016).

The quantitative nature of mustard yield and its section would be useful in gaining knowledge about the type and intensity of hereditary change ability and its collaboration with climate. The relationship between circumstances and genotypes is especially interesting because, if inherited features are known and, for the most part, predictable in advance, they represent climate changes. Given this, it makes more sense to assess heritability while accounting for the entire range of variance by combining genotype and environment. This is because it permits choices that result in expectations of inherited development. "Cradled" OR uniform genotypes are those that can change their phenotypic state in response to ecological fluctuations and offer the best level of steady financial return (Allard and Bradshaw, 1964).

Genetic variety is essential in plant breeding; genetically distinct plants may be used in order to obtain the desired segregating generation recombination because hybrids between lines of diverse origins frequently exhibit more heterosis than hybrids between closely related strains. Genetic variability is crucial when developing an efficient

breeding programme for the enhancement of any crop species, such as Indian mustard. Germplasm, or the sum of diversity found in any crop species and relatives, is critical for exploitation in order to meet the majority of the shifting demands for improved crop types.

II. MATERIALS AND METHODS

During the 2022 Rabi season, the experiment was conducted in 50 genotypes at the Research Farm, Department of Agriculture, Mata Gujri College, Sri Fatehgarh Sahib, Punjab. Using a Randomized Block Design with three replications, fifty B. juncea genotypes were planted in the field with a 45 cm row-to-row spacing and a 15 cm plant-to-plant distance.

Five randomly selected plants were observed for twelve features, including days to first blooming, days to 50% flowering, Plant height (cm), number of siliqua per plant, number of seeds per siliqua, length of siliquae (cm), number of primary and secondary branches, days to maturity, biological yield (g), seed yield (g), and harvest index (%) are all included. Each character's test of significance was examined using the methods recommended by Panse and Sukhatme (1967).

Al-Jibouri et al. (1958) provided the formula for calculating the genotypic and phenotypic coefficients of variation, Burton and De Vane (1953) provided the broad definition of heritability (h2), and Johnson et al. (1955) proposed a procedure for calculating genetic advance, or the expected genetic gain.

III. RESULT AND DISCUSSION

3.1 Analysis of variance

Analysis of variance presented inclearly suggests that the significant differences among the genotypes for all traits indicating presence of significant genetic variability and diversity in the experimental material. All 12 variables, including days to first flowering, showed significant genotype differences, according to the analysis of variance. Plant height, number of siliquae/plants, siliqua length, number of seeds/siliquas, number of primary and secondary branches per plant, days to 50% flowering, and days to maturity. harvest index, biological yield, and seed yield/plant by Shekhawat et al. (2014) and Pant and Singh (2001).

3.2 Mean Performance

The highest and lowest mean performance of fifty genotypes for various characters has been described, and the results of these studies are presented is the appendix.

- 1. **Days to first flowering:** Mean value for 50 genotypes were ranging from **IC-589686** (65.00) to **Ashirwad** (82.00).
- 2. **Days to 50% flowering:** The average value of 50 genotypes were varies **from IC-571662** (74.00) to **IC-405235** (94.00).
- 3. **Days to maturity:** The average value of 50 genotypes were varies from **Jawahar Mustard** (121.00) to **IC-335852** (147.00).
- 4. Number of primary branches per plant: The mean value of 50 genotypes of mustard were varies from IC-405235 (2.40) to IC-311734 (9.40).
- 5. **Number of secondary branches per plant:** The mean value of 50 genotypes were ranging from **IC-405235** (6.00) to **IC-571678** (21.80).
- 6. **Plant height:** The highest and lowest mean performance of 50 genotypes were ranging from **IC-538719** (106.60) and **IC-599679** (170.40) respectively.
- 7. Silquae count per plant
- 8. : The mean value of 50 genotypes were ranging from for number of siliquae per plant is IC-589686 (47.80) to Navinder Roy (492.40).
- 9. **Siliqua length:** The lowest and highest mean performance of 50 genotypes for siliquae length is **IC-589681** (3.14) and **IC-355856** (4.92).
- 10. The number of seeds in each siliqua: The mean value of 50 genotypes for number of seed per siliquae were ranging from **Geeta** (8.00) to **IC-571661** (20.00).
- 11. **Biological yield:** The mean value of 50 genotypes for biological yield per plant were ranging from **IC-589681** (10.94) to **IC-405235** (191.72).
- 12. **Harvest index:** The minimum and the maximum value of mean performance for 50 genotypes for harvest index is **IC-339953** (8.33) and **IC-599679** (54.48).
- 13. **Seed yield per plant:** The mean value of 50 genotypes for seed yield per plant were ranging from **IC-589681**(3.54) to **IC-571630** (49.32).

3.3 Variability and Genetic Parameters

Analysis of Variance demonstrated that for every character under study, the mean sum of squares resulting from genotypes was significant. Significant genetic variability is indicated by a very significant connection. The values of the phenotypic coefficient of variation (PCV), genotypic coefficient of variation, and environmental coefficient of variation are found in Table 1.1, which also presents estimates of the various genetic parameters. The data showed that, for the majority of de

min, PCV was more significant than GCV. The highest PCV and GCV values (194.29 and 172.87) were found in the number of siliquae per plant. For every seed quality criterion, the phenotypic coefficients of variation (PCV) were somewhat greater than the corresponding genotypic coefficients of variation due to environmental effect.

The identical outcomes were also reported by Chaudhary *et al.* (2003), Akabari and Niranjana (2015), Dilip et al. (2016), Srivastava *et al.* (2016) and Hyder *et al.* (2021). Similar results were found by Singh *et al.* (2018), Pant and Singh (2001), Shekhawat *et.al* (2014).

3.4 Heritability Genetic advance

Heritability enhances selection effectiveness by separating experimental influence from total variability. The number of seeds per siliquae (95.83), days to 50% blooming (95.28), number of secondary branches (94.01), biological yield (89.64), harvest index (87.03), and siliqua length (82.64) were among the plant growth parameters where high heritability was noted. Singh (2004), Kumar and Misra (2007), and Yadava et al. (2011) all noted similar results. The high estimates of heritability values indicated that a considerable portion of the phenotypic variability for the feature in issue was heritable. Therefore, easy selection would be beneficial for increasing these traits.

According to the study, the number of siliquae per plant (104.77) had the greatest estimate of genetic advancement, followed by the number of secondary branches (101.73), the number of seeds per siliqua (91.45), the height of the plant (78.23), the biological yield (65.78), and the number of days of 50% blooming (63.48). The scope of improvement by simple selection was limited by the lowest estimates for the number of primary branches (5.66), siliquae length (7.21), and seed yield (7.27), as well as the number of days until first flowering (10.65). Additive gene activity is suggested by high heritability and genetic advancement in certain characteristics. Genetic advancement and moderate heritability, on the other hand, are controlled by both additive and non-additive gene activity but exhibit less environmental effect.

With variables like plant height and siliqua length exhibiting low heritability and genetic advance values, selection in succeeding generations may result in only little improvement. Singh et al. (2011) reported similar results. Additionally, all of these traits had substantial estimates of heritability. For several siliqua/plants, such high heritability along with high genetic advancement has been shown. Similar result has been reported by Singh *et al.* (2012) and Tiwari *et al.* (2016).

Table 1 Analysis of variance for yield and yield traits in 50 genotypes of Indian mustard (Brassica juncea L)

Source of Variation	DF	Days of first flowering	Days of 50% Flowering	No. of primary branches	No of Secondary branches	Plant Height (cm)	No. of Seeds/ siliquae	Siliquae length (cm)	No. of Seeds/siliquae	Days of Maturity	Biological yield/ plant (g)	Seed yield/ plant (g)	Harvest index (%)
Replication	2	154.94	60.927	55.553	1,691.96	37,443.98	86.087	86.717	86.087	2,388.29	499.457	25.254	17.968
Treatment	49	108.173	3,039.68	40.672	7,947.90	11,361.14	6,260.02	47.531	6,260.02	2,991.13	3,543.56	98.574	1,474.92
Error	98	8.239	49.355	6.093	165.191	2,796.84	89.59	3.11	89.59	290.699	131.434	24.361	69.789

Characters	Maar	Range		GCV(%)	PCV(%)	Heritability	GA	GA%	
Characters	Mean	Min Max		GCV(%)	PCV(%)	Heritability	GA	mean	
Days to first flowering	84.48	65.00 82.00		6.832	7.63	80.17	10.65	12.60	
Days to 50% flowering	22.15	74.00	94.00	142.55	146.04	95.28	63.48	286.66	
Primary Branches Number	12.89	2.40	9.40	26.34	32.56	65.42	5.66	43.88	
Secondary branches Number	118.78	6.00	21.80	42.88	44.22	94.01	101.73	85.65	
Plant Height (cm)	187.67	106.60	170.40	28.47	40.057	50.51	78.23	41.68	
No. of Siliquae/ plant	33.06	47.80	492.40	172.87	194.29	79.17	104.77	316.86	
Siliquae length (cm)	12.24	3.14	4.92	31.43	34.57	82.64	7.21	58.86	
No. of Seeds / siliquae	108.89	8.00	20.00	41.65	42.54	95.83	91.45	83.99	
Days of Maturity	97.25	125.00	137.33	30.85	35.48	75.59	53.73	55.25	
Biological yield/ plant	30.78	42.61	150.98	109.55	115.70	89.64	65.78	213.67	
Seed yield/ plant	18.83	8.85	40.54	26.41	37.21	50.38	7.27	38.62	
Harvest index (%)	63.68	9.97	33.03	33.99	36.43	87.03	41.59	65.31	

Table 2 Estimation of different genetic parameters of variation for 12 traits among parents

IV. CONCLUSION

The results of present study indicated that ample amount of genetic variability present in the material. The mean performance of 50 genotypes for various characters was analysed, highlighting the highest and lowest mean performances across different traits. The coefficient of variation was used to indicate the extent of variability present for these traits. Analysis of genetic parameters revealed that in most cases, the broad sense heritability (PCV) had a higher effect compared to the narrow sense heritability (GCV). Traits such as number of siliquae per plant, days to 50% flowering, biological yield, number of secondary branches per plant, number of seed per siliqua, plant height, seed yield per plant, harvest index, days to maturity, siliqua length, number of primary branches per plant, and days to first flowering exhibited the highest values of PCV and GCV.

REFERENCES

- Akabari VR and Niranjana M (2015). Genetic variability and trait association studies in Indian mustard (*Brassica juncea* L). *International Journal of Agricultural Sciences* 1(11): 35-39
- [2] Al-Jibouri, H. A., Miller and H. F. Robinson (1958). Genotypic and environmental variation and correlation in upland cotton cross of interspecies origin. Agron, J. 50: 633-637.
- [3] Allard RM and Bradshaw AD (1964) Implication of genotype- environment interaction in applied plant breeding. *Crop Science* 4:503-508
- [4] Burton GW and Devane EH(1953) Estimating heritability in tall fesscusce from Replicated clone natural materials. Agronomy Journal 45:171-181
- [5] Burton, GW and Devane, EH (1953). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*, 45: 478-481
- [6] Chaudhary, VK, Kumar R, and Sah JN(2003). Variability studies in Indian mustard. *J.Appl.Bio*.13(1/2): 9-12.

- [7] Dilip, Shyam T, Singh, SK. and Kumar R (2016). Genetic Variability, Character Association and Path Analysis in Indian mustard. A Journal of Multidisciplinary Advance Research, 5(1): 50-58.
- [8] Hyder A, Iqbal A, Sheikh FA, Wani MA, Nagoo S, Khan M H, Dar, Z A, ul-Nisa, V and Ali G (2021). Genetic variability studies for yield and yield attributing traits in Gobhi Sarson (*Brassica napus* L.) genotypes under temperate ecology of Kashmir. *Journal of Oilseed Brassica*. 12(1): 44-48.
- [9] Johnson H W. Robinson, HF and Comstock RE (1995). Genotypic and phenotypic correlations and their implication in selection. *Agronomy Journal* 47(10): 477-483.
- [10] Kumar Satyendra, Misra MN (2007). Study on genetic variability, heritability and genetic advance in populations in Indian mustard (*Brassica juncea* L. Czern & Coss.). *International Journal of Plant Sciences*. 2(1):188-90
- [11] Mehla, HR., Jambhukar, SJ., Yadav, OK. and Sharma R (2003). Genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern and Coss) *Journal* of Genetics & Plant. Breeding 63(2): 171-172.
- [12] Panse VG and Sukhatme PV(1967). Statistical Method for Agricultural Workers, Second Edition. Indian Council of Agricultural Research New Delhi.
- [13] Pant SC and Singh P (2021). Genetic variability in Indian mustard. *Agricultural Science Digest* 21(1): 28-30.
- [14] Rao P, Avtar R, Kumari N, Jattan M, Rani B, Manmohan, Sheoran RK (2017). Multivariate analysis in Indian mustard genotypes for morphological and quality traits. *Electronic Journal of Plant Breeding* 8(2): 450-458
- [15] Saleem N, Jan SA, Atif MJ, Khurshid H, Khan SA and Abdullah M (2017). Multivariate based variability within diverse Indian mustard (B. *juncea* L.) genotypes. *Open Journal of Genetics*;7:(69-83)
- [16] Sharma B, Kumari P, Kumari R, Tripathi SK, Kumar A, Dhara PK (2020). Impact of Multistorey System on yield and Soil Quality of Mustard in Alfisols of Eastern India. Adrri Journal of Agriculture and Food sciences 4(6)1-20
- [17] Shekhawat N, Jadeja G C and Singh J. (2014). Genetic variability for yield and its components in Indian mustard (*Brassica juncea* L. Czern & Coss). *Electronic Journal of Plant Breeding* 5(1): 117-119
- [18] Shrimali TM, Chauhan RM, Gami RA and Patel PT (2016). Diallel analysis in Indian mustard [Brassica juncea L. (Czern & Coss.)]. Electronic Journal of Plant Breeding, 7(4): 919-
- [19] Singh B (2004). Character association and path analysis under dry land condition in Indian mustard (*Brassica juncea* L.). Cruciferae Newsletter.25:99-100.
- [20] Singh D K. Kumar K and Singh P (2012). Heterosis and heritability analysis for different crosses in *Brassica juncea* with inheritance of white rust resistance. *Journal of Oilseed Brassica* 3(1): 18-26
- [21] Singh K. Singh D and Singh AK (2012). Genetic divergence for important economic and quality traits in Indian mustard (*Brassica juncea L*) Pantnagar Journal of Research 9(2): 183-188
- [22] Singh S, Dwivedi AK, Ashutosh, Meena O, Kumar K (2018). Genotypic variability, Heritability and genetic advance in

- Indian mustard [Brassica juncea (L.) Czern & Coss.] Genotypes. Journal of Pharmacognosy and Phytochemistry 7(3):350-352
- [23] Srivastava KK, Vimal SC, Giri SP and Verma AK (2016). Studies on seed quality parameters in Indian mustard (*Brassica juncea* L.). *Indian Journal of Agricultural Sciences*, 12 (2): 241-244.
- [24] Tiwari AK, Singh AK, Tomar and Singh M (2016). Heritability, genetic advance and correlation coefficient analysis in Indian mustard [Brassica juncea L. Czern and Coss.] Journal of Pharmacognosy and Phytochemistry 6(1): 356-359.
- [25] Yadava DK, Giri SC, Vignesh M, Vasudev S, Yadav AK, Dass B (2011). Genetic variability and trait association studies in Indian mustard (*Brassica juncea L.*). *Indian Journal of Agricultural Science*. 81(8):712-71